Exhibit 3 (handwritten)

NCBI	Entrez	BLAST 2 sequences	BLAST	Example	Help

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using __BLAST__ engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from __NCBI ftp site__
Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

__Program__ [blastn ▼] __Matrix__ [Not Applicable ▼]

Parameters used in __BLASTN__ program only:
Reward for a match: [1]   **Penalty for a mismatch:** [-2]
☐ Use __Mega BLAST__   Strand option [Both strands ▼]

Open gap [5] and extension gap [2] penalties
gap x_dropoff [5)] expect [10] word size [11] Filter ☑

Sequence 1 Enter accession or GI [13027635] or download from file [   ] [Browse...]
or sequence in FASTA format from: [   ] to: [   ]

[   ]

[Browse...]
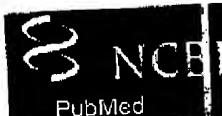
Sequence 2 Enter accession or GI [   ] or download from file [   ]
or sequence in FASTA format from: [   ] to: [   ]

[cgaccaagtctagagcgcttccggt   ]

[Align] [Clear] [Input]

Blast 2 Sequences results

NCBI

PubMed | Entrez | BLAST | OMIM | Taxonomy | Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.2 [Dec-14-2001]

Match: 1   Mismatch: -2   gap open: 5   gap extension: 2

x_dropoff: 50   expect: 10.000   wordsize: 11   Filter ☑   [Align]

Sequence 1	gi 130⁣7635	Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA	Length 2753
Sequence 2	lcl|seq_2		Length 25

No significant similarity was found